



SEQUENCE LISTING

#3

(1) GENERAL INFORMATION:

(i) APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki

(ii) TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS

(iii) NUMBER OF SEQUENCES: 132

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/646,265  
(B) FILING DATE: 09-SEP-1996  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/JP94/01763  
(B) FILING DATE: 19-OCT-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 5-291078  
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(C) REFERENCE/DOCKET NUMBER: 53466/184

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

40

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT

39

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSQTTG

40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

43

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC

40

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTAGTCGAC ATGAGGTKCY YTGYSAGYT YCTGRGG

37

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTCAATT G

41

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG

35

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC

38

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGATCCCGGG TGGATGGTGG GAAGATG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTAGTCGAC ATGAAATGCA GCTGGGTCAT STTCTTC

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT

36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTAGTCGAC ATGAAGWTGT GGTAAACTG GGTTTT

37

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTAGTCGAC ATGRACCTTTG GGYTCAGCTT GRTTT

35

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTAGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCCTT

40

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC

37

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT

36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG

37

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACTAGTCGAC ATGGATTTTG GGCTGATTTT TTTTATTG

38

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG

37

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATCCCGGG CCAGTGGATA GACAGATG

28

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG GAG TCA CAT ATT CAG GTC TTT GTA TAC ATG TTG CTG TGG TTG TCT 48  
Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser  
1 5 10 15

GGT GTT GAT GGA GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC 96  
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser  
20 25 30

ACA TCA GTA GGA GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT CAG AAT 144  
Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn  
35 40 45

GTG GGT ACT AAT GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT 192  
Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro  
50 55 60

AAA CCA CTG ATT TAC TCG GCA TCC TAT CGG TAC AGT GGA GTC CCT GAT 240  
Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp  
65 70 75 80

CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC ACC 288  
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr  
85 90 95

AAT GTG CAG TCT GAA GAC TTG GCA GAC TAT TTC TGT CAG CAA TAT AAC 336  
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn  
100 105 110

AGC TAT CCT CGG GCG TTC GGT GGA GGC ACC AAA CTG GAA ATC AAA 381  
Ser Tyr Pro Arg Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
115 120 125

C 382

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser  
1 5 10 15

Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser  
20 25 30

Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn  
35 40 45

Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro  
50 55 60

Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp  
65 70 75 80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr  
85 90 95

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn  
100 105 110

Ser Tyr Pro Arg Ala Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG 48  
Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly  
1 5 10 15

GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG 96  
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys  
20 25 30

CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT 144  
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile  
35 40 45

AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG 192  
Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu  
50 55 60

GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240  
Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp  
65 70 75 80

CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC 288  
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn  
85 90 95

ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC	336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val	
100 105 110	
TAT TAC TGT GCT TCG GCC TAC TAT GTT AAC CAG GAC TAC TGG GGT CAA	384
Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln	
115 120 125	
GGA ACC TCA GTC ACC GTC TCC TCA G	409
Gly Thr Ser Val Thr Val Ser Ser	
130 135	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly  
1 5 10 15

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys  
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile  
35 40 45

Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu  
50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp  
65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn  
85 90 95

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln  
115 120 125

Gly Thr Ser Val Thr Val Ser Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC

34

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGCGGATCCA CTCACGTTTG ATTTCCAGTT TGGT

34

(2) INFORMATION FOR SEQ ID NO:32:

- B1
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 43 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT

43

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA

34

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAGACAGTGG TTCAAAGT

18

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCGGAT CCACTCACGT TTGATT

26

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC

44

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG

38

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG

47

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC

44

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG

47

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGATAGCTGT TATATTGCTG GCAGTAGTAG GTAGCGATGT CCTC

44

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C

379

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
 -19                      -15                      -10                      -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
                          1                                      5                                      10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
                          15                                      20                                      25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
                          30                                      35                                      40                                      45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
    50                                      55                                      60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
    65                                      70                                      75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
    80                                      85                                      90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
    95                                      100                                      105

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTACCGACT ACACCTTCAC CATCAGCAGC C

31

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A

31

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGT GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

378

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379

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser  
65 70 75  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCTACCTACT TCTGCCAGCA ATATAACAG

29

(2) INFORMATION FOR SEQ ID NO:49:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGCTGGCAGA AGTAGGTAGC GATGTCCTC

29

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..378

(ix) FEATURE:

- ```
(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..378
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C 379

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C 379

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser  
65 70 75  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TGACAGAGTG TCCGTCACCT GTAAGGCCA

29

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTACAGGTGA CGGACACTCT GTCACCCAC

29

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C 379

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Trp | Ser | Cys | Ile | Ile | Leu | Ser | Leu | Val | Ala | Thr | Ala | Thr | Gly |  |
| -19 |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     | -5  |  |
| Val | His | Ser | Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala |  |
|     |     |     | 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |  |
| Ser | Val | Gly | Asp | Arg | Val | Ser | Val | Thr | Cys | Lys | Ala | Ser | Gln | Asn | Val |  |
|     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |  |
| Gly | Thr | Asn | Val | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys |  |
| 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |
| Leu | Leu | Ile | Tyr | Ser | Ala | Ser | Tyr | Arg | Tyr | Ser | Gly | Val | Pro | Ser | Arg |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |  |
| Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Phe | Thr | Ile | Ser | Ser |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |  |
| Leu | Gln | Pro | Glu | Asp | Ile | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Tyr | Asn | Ser |  |
|     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |  |
| Tyr | Pro | Arg | Ala | Phe | Gly | Gln | Gly | Thr | Lys | Val | Glu | Ile | Lys |     |     |  |
|     | 95  |     |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TCC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | 48  |
| Met | Gly | Trp | Ser | Cys | Ile | Ile | Leu | Ser | Leu | Val | Ala | Thr | Ala | Thr | Gly |     |
| -19 |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     | -5  |     |
| GTC | CAC | TCC | GAC | ATC | CAG | ATG | ACC | CAG | AGC | CCA | AGC | AGC | CTG | AGC | GCC | 96  |
| Val | His | Ser | Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala |     |
|     |     |     | 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |
| AGC | GTG | GGT | GAC | AGA | GTG | TCC | GTC | ACC | TGT | AAG | GCC | AGT | CAG | AAT | GTG | 144 |
| Ser | Val | Gly | Asp | Arg | Val | Ser | Val | Thr | Cys | Lys | Ala | Ser | Gln | Asn | Val |     |
|     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG | 192 |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys |     |
| 30 35 40 45                                                     |     |
| CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA | 240 |
| Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |     |
| 50 55 60                                                        |     |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |     |
| 65 70 75                                                        |     |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC | 336 |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser |     |
| 80 85 90                                                        |     |
| TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA         | 378 |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |     |
| 95 100 105                                                      |     |
| C                                                               | 379 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly |  |
| -19 -15 -10 -5                                                  |  |
| Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala |  |
| 1 5 10                                                          |  |
| Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val |  |
| 15 20 25                                                        |  |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys |  |
| 30 35 40 45                                                     |  |
| Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |  |
| 50 55 60                                                        |  |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |  |
| 65 70 75                                                        |  |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser |  |
| 80 85 90                                                        |  |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |  |
| 95 100 105                                                      |  |

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACTTCACCT TGACCATCAG CAGCCT

26

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTGCTGATGG TCAAGGTGAA GTCGGT

26

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

48

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

96

1

5

10

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG | 144 |
| Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val |     |
| 15 20 25                                                        |     |
| GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG | 192 |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys |     |
| 30 35 40 45                                                     |     |
| CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA | 240 |
| Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |     |
| 50 55 60                                                        |     |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser |     |
| 65 70 75                                                        |     |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC | 336 |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser |     |
| 80 85 90                                                        |     |
| TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA         | 378 |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |     |
| 95 100 105                                                      |     |
| C                                                               | 379 |

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly |  |
| -19 -15 -10 -5                                                  |  |
| Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala |  |
| 1 5 10                                                          |  |
| Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val |  |
| 15 20 25                                                        |  |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys |  |
| 30 35 40 45                                                     |  |
| Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |  |
| 50 55 60                                                        |  |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser |  |
| 65 70 75                                                        |  |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser |  |
| 80 85 90                                                        |  |

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C

379

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19                      -15                      -10                      -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
                    1                      5                      10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
         15                      20                      25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30                      35                      40                      45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
                    50                      55                      60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
                    65                      70                      75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
                    80                      85                      90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95                      100                      105

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGACAGAGTC CAAAGCCGCT GATCTACTC

29

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATCAGCGGCT TTGGACTCTG TCCTGGCTT

29

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40 45

CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

378

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379

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40 45  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAGGACATCG CTGACTACTT CTGCCA

26

(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:71:

AAGTAGTCAG CGATGTCCTC TGGCTG

26.

## (2) INFORMATION FOR SEQ ID NO:72:

(A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS  
(B) LOCATION: 1..378

```
(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..378
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TCC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | 48  |
| Met | Gly | Trp | Ser | Cys | Ile | Ile | Leu | Ser | Leu | Val | Ala | Thr | Ala | Thr | Gly |     |
| -19 |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     | -5  |     |
| GTC | CAC | TCC | GAC | ATC | CAG | ATG | ACC | CAG | AGC | CCA | AGC | AGC | CTG | AGC | GCC | 96  |
| Val | His | Ser | Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala |     |
|     |     |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |
| AGC | GTG | GGT | GAC | AGA | GTG | TCC | GTC | ACC | TGT | AAG | GCC | AGT | CAG | AAT | GTG | 144 |
| Ser | Val | Gly | Asp | Arg | Val | Ser | Val | Thr | Cys | Lys | Ala | Ser | Gln | Asn | Val |     |
|     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |
| GGT | ACT | AAT | GTA | GCC | TGG | TAC | CAG | CAG | AAG | CCA | GGA | CAG | AGT | CCA | AAG | 192 |
| Gly | Thr | Asn | Val | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Lys |     |
| 30  |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| CCG | CTG | ATC | TAC | TCG | GCA | TCC | TAT | CGG | TAC | AGT | GGT | GTG | CCA | AGC | AGA | 240 |
| Pro | Leu | Ile | Tyr | Ser | Ala | Ser | Tyr | Arg | Tyr | Ser | Gly | Val | Pro | Ser | Arg |     |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| TTC | AGC | GGT | AGC | GGT | AGC | GGT | ACC | GAC | TTC | ACC | TTG | ACC | ATC | AGC | AGC | 288 |
| Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser |     |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |

CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C 379

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40 45  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75  
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C 379

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75

Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40 45

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA | 240 |
| Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |     |
| 50 55 60                                                        |     |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |     |
| 65 70 75                                                        |     |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC | 336 |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser |     |
| 80 85 90                                                        |     |
| TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA         | 378 |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |     |
| 95 100 105                                                      |     |
| C                                                               | 379 |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGAGCCAAA AGTTCCTGAG CGCCAG

26

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTCAGGAACT TTTGGCTCTG GGTCAT

26

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ATG | GGA | TGG | AGC | TGT | ATC | ATC | CTC | TCC | TTG | GTA | GCA | ACA | GCT | ACA | GGT | 48 |
| Met | Gly | Trp | Ser | Cys | Ile | Ile | Leu | Ser | Leu | Val | Ala | Thr | Ala | Thr | Gly |    |
| -19 |     |     |     | -15 |     |     |     |     | -10 |     |     |     |     |     | -5  |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| GTC | CAC | TCC | GAC | ATC | CAG | ATG | ACC | CAG | AGC | CAA | AAG | TTC | CTG | AGC | GCC | 96 |
| Val | His | Ser | Asp | Ile | Gln | Met | Thr | Gln | Ser | Gln | Lys | Phe | Leu | Ser | Ala |    |
|     |     |     | 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGC | GTG | GGT | GAC | AGA | GTG | ACC | ATC | ACC | TGT | AAG | GCC | AGT | CAG | AAT | GTG | 144 |
| Ser | Val | Gly | Asp | Arg | Val | Thr | Ile | Thr | Cys | Lys | Ala | Ser | Gln | Asn | Val |     |
|     | 15  |     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG | 192 |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys |     |
| 30 35 40 45                                                     |     |
| CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA | 240 |
| Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |     |
| 50 55 60                                                        |     |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |     |
| 65 70 75                                                        |     |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC | 336 |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser |     |
| 80 85 90                                                        |     |
| TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA         | 378 |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |     |
| 95 100 105                                                      |     |
| C                                                               | 379 |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly |  |
| -19 -15 -10 -5                                                  |  |
| Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala |  |
| 1 5 10                                                          |  |
| Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val |  |
| 15 20 25                                                        |  |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys |  |
| 30 35 40 45                                                     |  |
| Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |  |
| 50 55 60                                                        |  |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |  |
| 65 70 75                                                        |  |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser |  |
| 80 85 90                                                        |  |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |  |
| 95 100 105                                                      |  |

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGACAGAGTC CAAAGCTGCT GATCTACTC

29

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATCAGCAGCT TTGGACTCTG TCCTGGCTT

29

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT  
 Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
 -19 -15 -10 -5

48

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC  
 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
 1 5 10

96

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG | 144 |
| Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val |     |
| 15 20 25                                                        |     |
| GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG | 192 |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys |     |
| 30 35 40 45                                                     |     |
| CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA | 240 |
| Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |     |
| 50 55 60                                                        |     |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |     |
| 65 70 75                                                        |     |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC | 336 |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser |     |
| 80 85 90                                                        |     |
| TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA         | 378 |
| Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys         |     |
| 95 100 105                                                      |     |
| C                                                               | 379 |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly |  |
| -19 -15 -10 -5                                                  |  |
| Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala |  |
| 1 5 10                                                          |  |
| Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val |  |
| 15 20 25                                                        |  |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys |  |
| 30 35 40 45                                                     |  |
| Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |  |
| 50 55 60                                                        |  |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |  |
| 65 70 75                                                        |  |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser |  |
| 80 85 90                                                        |  |

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40 45

CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA 378  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

C

379

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
 -19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
 50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 95 100 105

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCTCCAAAGC CGCTGATCTA CTC

23

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TAGATCAGCG GCTTTGGAGC CTT

23

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT | 48  |
| Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly |     |
| -19 -15 -10 -5                                                  |     |
| GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC | 96  |
| Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala |     |
| 1 5 10                                                          |     |
| AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG | 144 |
| Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val |     |
| 15 20 25                                                        |     |
| GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG | 192 |
| Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys |     |
| 30 35 40 45                                                     |     |
| CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA | 240 |
| Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg |     |
| 50 55 60                                                        |     |
| TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC | 288 |
| Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser |     |
| 65 70 75                                                        |     |
| CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC | 336 |
| Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser |     |
| 80 85 90                                                        |     |

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

378

C

379

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
1 5 10  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40 45  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
50 55 60  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

AAGAAGCCTG GGTCTCAGT GAAGGTCTCC TGCAAGGCTT CTGGCTTCAA CATTAAAGAC 60  
ACCTATATAC ACTGGGTGCG CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAGGATT 120

GATCCTGAGG ATGGTAA

137

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGAGATCTGA GGACACAGCC TTTTATTTCT GTGCAAGTGC CTACTATGTT AACCAGGACT 60  
ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C 111

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 130 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ACCTTCACTG AGGACCCAGG CTTCTTCACC TCAGCTCCAG ACTGCACCAG CTGCACCTGG 60  
GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCCAGGTCCA GTCCATGGTC 120  
GAAGCTTATC 130

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTC 60  
GTCTGCAGTG ATTGTGACTC GGCCCTGGAA CTTCGGGTCA TATTTAGTAT TACCATCCGC 120

AGGATCAATC CT

132

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATAAGCTTC CACCATGGAC TGGAC

25

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTCGGATCCA CTCACCTGAG GAGAC

25

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 409 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT GTA GCT CCA GGT  
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly  
-19 -15 -10 -5

48

GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG GTG AAG AAG 96  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10  
 CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC TTC AAC ATT 144  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile  
 15 20 25  
 AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA CAG GGC CTG 192  
 Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 GAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240  
 Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp  
 50 55 60  
 CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA TCC ACG AAC 288  
 Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn  
 65 70 75  
 ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACA GCC TTT 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe  
 80 85 90  
 TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC TGG GGC CAA 384  
 Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln  
 95 100 105  
 GGG ACC ACT GTC ACC GTC TCC TCA G 409  
 Gly Thr Thr Val Thr Val Ser Ser  
 110 115

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly  
 -19 -15 -10 -5  
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile  
 15 20 25  
 Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp  
 50 55 60

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn  
65 70 75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe  
80 85 90

Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln  
95 100 105

Gly Thr Thr Val Thr Val Ser Ser  
110 115

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AGCTTGTCAC CGTCTCCTCA GGTGGTGGTG GTTCGGGTGG TGGTGGTTCG GGTGGTGGCG 60  
GATCGGACAT CCAGATGACC CAGG 84

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AATTCCTGGG CCATCTGGAT GTCCGATCCG CCACCACCCG AACCACCACC ACCCGAACCA 60  
CCACCACCTG AGGAGACGGT GACA 84

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG

34

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCACCCGAAC CACCACCACC TGAGGAGACG GTGACAGTGG T

41

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G

41

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A

41

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG

44

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CAAGAATTCT TATTATTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT

57

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..807

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT  
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15

48

GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG  
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu  
20 25 30

96

GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC  
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  
35 40 45

144

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| TTC AAC ATT AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA<br>Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly<br>50 55 60        | 192 |
| CAG GGC CTG GAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT<br>Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr<br>65 70 75 80     | 240 |
| AAA TAT GAC CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA<br>Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu<br>85 90 95        | 288 |
| TCC ACG AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC<br>Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp<br>100 105 110     | 336 |
| ACA GCC TTT TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC<br>Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr<br>115 120 125     | 384 |
| TGG GGC CAA GGG ACC ACT GTC ACC GTC TCC TCA GGT GGT GGT GGT TCG<br>Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser<br>130 135 140     | 432 |
| GGT GGT GGT GGT TCG GGT GGT GGC GGA TCG GAC ATC CAG ATG ACC CAG<br>Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln<br>145 150 155 160 | 480 |
| AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC<br>Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr<br>165 170 175     | 528 |
| TGT AAG GCC AGT CAG AAT GTG GGT ACT AAT GTA GCC TGG TAC CAG CAG<br>Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln<br>180 185 190     | 576 |
| AAG CCA GGA AAG GCT CCA AAG CCG CTG ATC TAC TCG GCA TCC TAT CGG<br>Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg<br>195 200 205     | 624 |
| TAC AGT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC<br>Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp<br>210 215 220     | 672 |
| TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC<br>Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr<br>225 230 235 240 | 720 |
| TAC TGC CAG CAA TAT AAC AGC TAT CCT CGG GCG TTC GGC CAA GGG ACC<br>Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr<br>245 250 255     | 768 |
| AAG GTC GAA ATC AAA GAC TAC AAA GAC GAT GAC GAT AAA TAATAAGAAT<br>Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Lys<br>260 265                          | 817 |
| TCTTG                                                                                                                                                 | 822 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala  
1 5 10 15  
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu  
20 25 30  
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  
35 40 45  
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly  
50 55 60  
Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr  
65 70 75 80  
Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu  
85 90 95  
Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp  
100 105 110  
Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr  
115 120 125  
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
130 135 140  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln  
145 150 155 160  
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr  
165 170 175  
Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln  
180 185 190  
Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg  
195 200 205  
Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
210 215 220  
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr  
225 230 235 240  
Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr  
245 250 255

Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Lys  
260 265

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..45

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGT GGT GGT GGT TCG GGT GGT GGT GGT TCG GGT GGT GGC GGA TCG  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

45

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
 20 25 30  
 Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro  
 35 40 45  
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile  
 50 55 60  
 Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Phe Gly Gln  
 65 70 75 80  
 Gly Thr Lys Val Glu Ile Lys  
 85

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Trp Val  
 20 25 30  
 Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Val Thr Ile  
 35 40 45  
 Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu  
 50 55 60  
 Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Gly  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Thr Tyr Ile His  
1 5

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln  
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Tyr Tyr Val Asn Gln Asp Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ser Ala Ser Tyr Arg Tyr Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Gln Gln Tyr Asn Ser Tyr Pro Arg Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1                      5                      10                      15  
Asp Arg Val Thr Ile Thr Cys  
20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
1                      5                      10                      15  
Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys  
20                      25                      30

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys  
20 25 30

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu  
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Ser  
20 25 30

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile  
 35 40 45  
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg  
 85 90 95  
 Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile  
 35 40 45  
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg  
 85 90 95  
 Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
 100 105

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr  
20 25 30  
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45  
Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe  
50 55 60  
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
85 90 95  
Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110  
Val Thr Val Ser Ser  
115

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